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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=28; hr=18; min=44; sec=17; ms=808;]

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Reviewer Comments:

<150> Polynucleotides and Polypeptides in Plants

<151> 2003-09-18

The above <150> response is invalid: per Sequence Rules, the only response to <150> can be a prior or related application number, not an invention title.

<210> 113

<211> 102

<212> PRT

<213> artificial sequence

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<221> misc_feature

<222> (2)..(2)

<223> Xaa can be any naturally occurring amino acid

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<223> Figs 6A-6C consensus sequence, where X is any amino acid and the
1st X is is no amino acid or A, P, G, S or T, 2nd X is 0-17 residues,
3rd X is 0-32 residues, 4th X is K, R, N or Q, 5th X is no residue or P,
6th X is V, I, L, M, or A, 7th X is H, Q, N, A, M or C, 8th X is R or K,
9th X is no residue or L, I, M, V, A, or T

<400> 113

Met Xaa Asp Xaa Gly Gly Xaa Glu Gln Asp Arg Phe Leu Pro Ile Ala
1 5 10 15

Asn Val Ser Arg Ile Met Lys Xaa Ala Leu Pro Ala Asn Ala Lys Ile
20 25 30

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
35 40 45

Ser Phe Ile Thr Xaa Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys
50 55 60

Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu
65 70 75 80

Gly Phe Glu Asp Tyr Xaa Glu Pro Leu Lys Val Tyr Leu Xaa Xaa Tyr
85 90 95

Arg Glu Xaa Glu Gly Glu
100

The above <223> response explaining "<213> Artificial Sequence" is insufficient: please give more information regarding the source of the genetic material. This error also occurs in Sequences 104-105, 107-108, and 113-115. Also, the above <223> response beginning "Figs 6A-6C consensus sequence" exceeds the Sequence Rules' required 72-character limit (this includes white spaces). Please insert hard returns, so that the lines do not exceed 72 characters. Per Sequence Rules, the <223> response has a maximum of 4 lines. If the response exceeds 4 lines, please insert a "<220>" above the 5th line, and insert a "<223>" at the beginning of the 5th line. This error also appears in other sequences.

Application No: 10675852 Version No: 3.0

Input Set:

Output Set:

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Finished: 2008-01-21 16:42:10.189
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 824 ms
Total Warnings: 8
Total Errors: 0
No. of SeqIDs Defined: 115
Actual SeqID Count: 115

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W 213	Artificial or Unknown found in <213> in SEQ ID (115)

SEQUENCE LISTING

<110> Mendel Biotechnology, Inc.
HEARD, Jacqueline E
KEDDIE, James S
CREELMAN, Robert A
PINEDA, Omaira
JIANG, Cai-Zhong
RATCLIFFE, Oliver
KUMIMOTO, Roderick
GUTTERSON, Neal
SHERMAN, Bradley K

<120> PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS

<130> MBI-0022CIP

<140> 10675852

<141> 2003-09-30

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<151> 2003-04-10

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<151> 2000-03-22

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<151> 1999-03-23

<150> 09/713,994

<151> 2000-11-16

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<151> 1999-11-17

<150> 10/112,887

<151> 2002-03-18

<150> 10/286,264

<151> 2003-01-23

<150> 10/225,068

<151> 2002-08-09

<150> 10/225,066

<151> 2002-08-09

<150> 10/374,780

<151> 2003-02-25

<150> 09/837,944

<151> 2001-04-18

<150> 10/171,468

<151> 2002-06-14

<150> 60/310,847
 <151> 2001-08-09

<150> 60/336,049
 <151> 2001-11-19

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 <151> 2003-09-18

<150> 60/434,166
 <151> 2002-12-17

<150> 60/411,837
 <151> 2002-09-18

<160> 115

<170> PatentIn version 3.2

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Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
35 40 45

Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
100 105 110

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65 70 75 80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
85 90 95

Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln
100 105 110

Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
115 120 125

Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly
130 135 140

Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His
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Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp

35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile

50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile

65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp

85 90 95

Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Val Glu

100 105 110

Gly Glu Lys Thr Thr Thr Ala Gly Arg Gln Gly Asp Lys Glu Gly Gly

115 120 125

Gly Gly Gly Gly Gly Ala Gly Ser Gly Ser Gly Gly Ala Pro Met Tyr

130 135 140

Gly Gly Gly Met Val Thr Thr Met Gly His Gln Phe Ser His His Phe

145 150 155 160

Ser

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<212> DNA
<213> Arabidopsis thaliana

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<223> G1364

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agccgtatca tgaaaagagg tcttctctgct aatgggaaaa tcgctaaaga tgctaaggag 180

attgtgcagg aatgtgtctc tgaattcatc agtttcgtca ccagcgaagc gagtgataaa 240

tgtcaaagag agaaaaggaa gactattaat ggagatgatt tgctttgggc aatggctact 300

ttaggatttg aagactacat ggaacctctc aaggtttacc tgatgagata tagagagggt 360

gacacaaagg gatcagcaaa aggtggggat ccaaagcaaa agaaagatgg gcaatcaagc 420

caaaatggcc agttctcgca gcttgcac caaggtcctt atgggaactc tcaagtaact 480

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Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu
35 40 45

Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Ile Val Gln Glu
50 55 60

Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys
65 70 75 80

Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp
85 90 95

Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Met Glu Pro Leu Lys Val
100 105 110

Tyr Leu Met Arg Tyr Arg Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly
115 120 125

Gly Asp Pro Asn Ala Lys Lys Asp Gly Gln Ser Ser Gln Asn Gly Gln
130 135 140

Phe Ser Gln Leu Ala His Gln Gly Pro Tyr Gly Asn Ser Gln Val Thr
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Phe Pro Leu Phe Ser Ser His Ser Ser Asn Thr His His Ser Leu Leu
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Ile Cys

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Gly Gly Asp Gln Ser Pro Arg Ser Leu Asn Val Arg Glu Gln Asp Arg
 20 25 30

Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu Pro
 35 40 45

Leu Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Met Gln Glu Cys
 50 55 60

Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys Cys
 65 70 75 80

Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala
 85 90 95

Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Asp Pro Leu Lys Val Tyr
 100 105 110

Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Gly Lys
 115 120 125

Gly Gly Glu Ser Ser Ala Lys Arg Asp Gly Gln Pro Ser Gln Val Ser
 130 135 140

Gln Phe Ser Gln Val Pro Gln Gln Gly Ser Phe Ser Gln Gly Pro Tyr

145 150 155 160

Gly Asn Ser Gln Ser Leu Arg Phe Gly Asn Ser Ile Glu His Leu Glu
165 170 175

Val Leu Met Ser Ser Thr Arg Thr Leu Phe Ile Thr Ile Phe Arg Asp
180 185 190

Ser Thr Met Pro Val Val Ser Glu Asn Leu Ser Asp Pro Leu Ser Ile
195 200 205

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Leu Ser Cys Lys
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20 25 30

Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Gly
35 40 45

Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50 55 60

Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr
85 90 95

Leu Gly Phe Glu Asp Tyr Met Asp Pro Leu Lys Ile Tyr Leu Thr Arg
100 105 110

Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly Gly Asp
115 120 125

Ser Ser Ala Lys Arg Asp Val Gln Pro Ser Pro Asn Ala Gln Leu Ala

130

135

140

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